

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 15:58:17 ; Search time 12.89 Seconds
(without alignments)
2030.348 Million cell updates/sec

Title: US-09-587-111-5

Perfect score: 4004
Sequence: 1 MTPSSSPVFRLETLDDGGE.....EDEDGASEENVYPVLLQSN 764

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215	5.4	973	1 TRP5_HUMAN	Q9UL62 homo sapien
2	198.5	5.0	1275	1 TRP_DROME	P19334 drosophila
3	197.5	4.9	1124	1 TRPL_DROME	P48994 drosophila
4	159	4.0	809	1 TRP1_MOUSE	O61056 mus musculus
5	151	3.8	3924	1 ANK2_HUMAN	O01484 homo sapien
6	150.5	3.8	793	1 TRP1_HUMAN	P48995 homo sapien
7	140	3.5	1862	1 ANK1_MOUSE	Q02357 mus musculus
8	139	3.5	848	1 TRP3_HUMAN	P13507 homo sapien
9	134.5	3.4	1880	1 ANK1_HUMAN	P16157 homo sapien
10	134.5	3.4	1401	1 LATA_LATMA	P23631 latrodectus
11	133.5	3.3	642	1 YAZA_SCHPO	O09701 schistosom
12	130	3.2	930	1 TRP6_MOUSE	O61143 mus musculus
13	129	3.2	1964	1 NTC4_MOUSE	P31695 mus musculus
14	128.5	3.2	1093	1 SWI4_YEAST	P25302 saccharomyc
15	124.5	3.1	2703	1 NOTC_DROME	P07207 drosophila
16	123.5	3.1	832	1 ANR3_HUMAN	P03017 homo sapien
17	123	3.1	500	1 CACT_DROME	O03017 drosophila
18	121.5	3.0	1503	1 TRP7_HUMAN	O94759 homo sapien
19	121	3.0	931	1 TRP6_HUMAN	O9Y210 homo sapien
20	120.5	3.0	741	1 RNSA_HUMAN	O05823 homo sapien
21	120.5	3.0	823	1 YNS2_CAEBL	P24566 caenorhabd
22	119.5	3.0	357	1 SH5A_RAT	P35364 rattus norv
23	119	3.0	657	1 RES2_SCHPO	P41412 schistosom
24	119	3.0	836	1 TRP3_MOUSE	O92357 mus musculus
25	117.5	2.9	613	1 XSV1_CAEBL	Q22566 caenorhabd
26	116	2.9	357	1 SH5A_MOUSE	P30966 mus musculus
27	115	2.9	1429	1 L112_CAEBL	P14585 caenorhabd
28	113	2.8	971	1 KBF1_MOUSE	P25759 mus musculus
29	112.5	2.8	806	1 PA26_HUMAN	O06733 homo sapien
30	112	2.8	1302	1 MDR5_DROME	O00748 drosophila
31	112	2.8	2318	1 NTC3_MOUSE	O61982 mus musculus
32	111.5	2.8	764	1 AKR1_YEAST	P39010 saccharomyc
33	111.5	2.8	1083	1 YIL2_YEAST	P40480 saccharomyc

34	111.5	2.8	2444	1 NTC1_HUMAN	P46531 homo sapien
35	111	2.8	637	1 RES1_SCHPO	P33520 schistosom
36	110.5	2.8	538	1 THIP_HAEIN	P44985 haemophilus
37	110.5	2.8	1431	1 DAPK_HUMAN	P53355 homo sapien
38	109.5	2.7	906	1 KBF2_CHICK	P88150 gallus gall
39	109.5	2.7	2353	1 CCAH_HUMAN	O05180 homo sapien
40	109.5	2.7	2531	1 NTC1_RAT	O07008 rattus norv
41	109	2.7	1873	1 CCAS_RABIT	P07293 oryctolagus
42	108.5	2.7	448	1 NU4M_ANOU	P33511 anopheles g
43	108.5	2.7	2437	1 NOTC_BRARE	P46530 brachydanio
44	107.5	2.7	614	1 GAAL_YEAST	P39012 saccharomyc
45	107.5	2.7	679	1 RNSA_MOUSE	O05921 mus musculus

ALIGNMENTS

RESULT	1	TRP5_HUMAN	STANDARD	PRT	973 AA
ID	TRP5_HUMAN				
AC	O9UL62;				
DT	01-OCT-2000 (Rel. 40, Created)				
DT	01-OCT-2000 (Rel. 40, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	TRANSIENT RECEPTOR POTENTIAL CHANNEL 5 (HTRP-5).				
GN	TRPC5 OR TRP5.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RP	[1]				
RN	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=99425273; PubMed=10493832;				
RA	Sossey-Alaoui K., Lyon J.A., Jones L., Abidi F.E., Hartung A.J.,				
RA	Hane B., Schwartz C.E., Stevenson R.E., Srivastava A.K.;				
RT	"Molecular cloning and characterization of TRPC5 (HTRP5), the human				
RT	homologue of a mouse brain receptor-activated capacitative Ca(2+)				
entry channel.";					
RL	Genomics 60:330-340(1999).				
CC	-1- FUNCTION: SUGGESTED TO MEDATE CAPACITATIVE CALCIUM ENTRY (CCE).				
CC	-1- SEEMS TO FORM A CALCIUM PERMEANT CHANNEL.				
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).				
CC	-1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.				
CC	-1- SIMILARITY: CONTAINS 2 ANK REPEATS.				
CC	-----				
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AF054568; AAF00002.1; -				
DR	InterPro: IPR002110; -				
DR	InterPro: IPR002111; -				
DR	InterPro: IPR002153; -				
DR	Pfam: PF00023; ank. 2.				
DR	PRINTS: PRO1097; TRANSMEMBRANE; Ion transport; Calcium channel;				
DR	IONIC channel; Transmembrane; Ion transport; Calcium channel;				
KW	ANK repeat; Repeat; Glycoprotein.				
FT	TRANSMEM 331 351				POTENTIAL.
FT	TRANSMEM 364 384				POTENTIAL.
FT	TRANSMEM 399 419				POTENTIAL.
FT	TRANSMEM 438 458				POTENTIAL.
FT	TRANSMEM 471 491				POTENTIAL.
FT	TRANSMEM 513 533				POTENTIAL.
FT	TRANSMEM 568 588				POTENTIAL.
FT	TRANSMEM 604 624				POTENTIAL.
FT	REPEAT 69 98				ANK 1.
FT	REPEAT 141 170				ANK 2.
FT	REPEAT 91 91				N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD 91 91				

FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 678 678 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 900 900 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 973 AA; 111411 MW; FBC8CBF17BE42166 CRC64;

Query Match 5.4%; Score 215; DB 1; Length 973;
 Best Local Similarity 20.5%; Pred. No. 1e-07;
 Matches 162; Conservative 115; Mismatches 278; Indels 234; Gaps 36;

QY 122 KAVLN-LKQGVNACILPLQIDDSGPNQPLVNAOCTDYRHSALHAIERSLQCVK 180
 DB 34 KALINAVEKGDYATVQALQDAEAIYNN-VINICMDPL-GRSALLAIEMENLEIME 87
 QY 181 LTVENGANV-----HARACGRFQGGGTCE--YFGEL-----211
 DB 88 LLINHSYVGDALLAIKRVGVAVELLISYRPSG--EKQVPTLMMDTQSEFPDIT 144
 QY 212 PLSLAATKQMDVSVYLE-----NPHQASLOATDSQGNVLAHLMWISDSAEINIAL 265
 DB 145 PIMLAHTNNEYELIKLVQKRVITPRHQ-----IRCNQCEVS-183
 QY 266 VTSMYGGLQAGARLCPYVLEDIRNLQDITPKLAKKEGKIEIFRHILORESGISHLS 325
 DB 184 -SSEVDSLRSR-----LNTYKALASPLALSEDPILTAFR--LQMEDKELSKVE 234
 QY 326 RKF-TEWCYGPVAVSLYDLASVDSCEANSVLEIAFH-----CK 363
 DB 235 NEKAREYEELSOQCKLFKADLLQOARSRELEIILNRDHSLEDPQKHDIAKLKVAL 294
 QY 364 SPHRHRVYLEPIKLLQAKW-----384
 DB 295 KYHQKEVQAPNCOQLATLWYDGPGRMRKHWVKLLTCTIGLEPMLSTAVLISPRS 354
 QY 385 -DLILPKFPLNLCN--LIYMFITAVAH--OPTLKKQAAPHKAEGVSMILTG 436
 DB 355 NLGLFKPKPKIKFCHTASYLTFELMLLASOHIVRTDLHVGQPPPTVVE--WMLLPW- 410
 QY 437 ILILGIVLYVGLW-YFRRHVFIMISFIDSYFELLFOALLTVVSGVLCFLAE-- 493
 DB 411 -VLGPIWKEIKEMDGTETIHDMMNLMDFAMNSLY--LATISLKIYAVKYNCS 463
 QY 494 -----WLPPLVSAL-----VLGMLNLVYTRGFQHTGIYSVMIOKYLDELLELL 540
 DB 464 RPREEMEMHPTLAEALFAISNLSLRLISLFTANSHPQISGRMLL-DILKFLF 522
 QY 541 IYIVFLFGFVALVLSQEAHREAPRGPRATESVQPMEOEDBGCAQYRGILLEASLEL 600
 DB 523 IYCLVLAEFANGLNOL-YFYETRAIDEPNCKGIR--CEKONNA--FSTLFEETLOSL 575
 QY 601 FKFTIGMGL-----AFQOLHFRGMVLLLLAYVLLTYLLNMLIAMSETVSVAT 654
 DB 576 FMSVFGILNLYVNVKARHETFEVGAT--MEGTYNVLSVLLMLIAMMNSYOLIA 633
 QY 655 DSKSINKLQK---ISVLE-----MENGVN--WCKRKORACVMT 669
 DB 634 HADIEKFKATKLMASYFDEGTLPPFNIIIPSKSFLYLGNNFNMTFCPKRD----- 686
 QY 690 VGRKPGSGRRCFVEEVNNAW--EQTLPTLCEBPSGAGVPTLENPLASPKDE- 747
 DB 687 ----PGRRRR-----NLSRTERNADSLIONOHVOEIVRLNRYVAAAIRSKT 734
 QY 748 -DGASEENY 755
 DB 735 HEGLTENF 743

DT 01-NOV-1995 (rel. 32, last sequence update)
 DT 01-OCT-2000 (rel. 40, last annotation update)
 DE TRANSIENT RECEPTOR POTENTIAL PROTEIN.
 GN TRP
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RX MEDLINE=90180449; PubMed=2516726;
 RA Montell C., Rubin G.M.;
 RT "Molecular characterization of the Drosophila trp locus: a putative
 RT integral membrane protein required for phototransduction.";
 RL Neuron 2:1313-1323(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148782; PubMed=2482778;
 RA Wong F., Schaefer E.L., Roop B.C., Lamendola J.N., Johnson-Seaton D.,
 RA Shao D.;
 RT "Proper function of the Drosophila trp gene product during pupal
 RT development is important for normal visual transduction in the
 RT adult.";
 RL Neuron 3:81-94(1989).
 RN [3]
 RP SEQUENCE OF 1126-1275 FROM N.A.
 RX MEDLINE=88042982; PubMed=3118483;
 RA Wong F., Yuh Z.T., Schaefer E.L., Roop B.C., Ally A.H.;
 RT "Overlapping transcription units in the transient receptor potential
 RT locus of Drosophila melanogaster.";
 RL Somat. Cell Mol. Genet. 13:661-669(1987).
 CC -1- FUNCTION: REQUIRED FOR PHOTOTRANSDUCTION. SUGGESTED TO MEDIATE
 CC CALCIUM ENTRY. SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT
 CC CHANNEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
 CC MEMBRANES OF THE PHOTORECEPTOR CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
 CC -----
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 CC -----
 CC EMBL: M34394; AAA28976.1; -
 CC EMBL: M21306; AAA56928.1; -
 CC EMBL: M18634; AAA28977.1; -
 CC PIR: J00092; J00092.
 CC PIR: J00015; J00015.
 CC Flybase: FBgn0003861; trp.
 CC InterPro: IPR002110; -
 CC InterPro: IPR002153; -
 CC Pfam: PF00023; ank; 1.
 CC PRINTS: PR01097; TRNSRECEPT.
 CC PROSITE: PS50088; ANK_REPEAT; 1.
 CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 CC Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW Vision; ANK repeat; Repeat.
 FT TRANSMEM 334 354 POTENTIAL.
 FT TRANSMEM 378 401 POTENTIAL.
 FT TRANSMEM 419 436 POTENTIAL.
 FT TRANSMEM 457 471 POTENTIAL.
 FT TRANSMEM 504 527 POTENTIAL.
 FT TRANSMEM 612 630 POTENTIAL.
 FT TRANSMEM 636 661 POTENTIAL.
 FT REPEAT 69 98 ANK 1.
 FT REPEAT 143 172 ANK 2.

FT CONFLICT 285 288 GORO -> ASSE (IN REF. 2).
 FT CONFLICT 326 329 RRQO -> POE (IN REF. 2).
 FT CONFLICT 365 374 KPEVETTHS -> NPLSSSRTP (IN REF. 2).
 FT CONFLICT 785 785 S -> N (IN REF. 2).
 SQ SEQUENCE 1275 AA; 142589 MW; 91CFCD986969B1 CRC64;

Query Match 5.0%; Score 198.5; DB 1; Length 1275;
 Best Local Similarity 19.9%; Pred. No. 2.2e-06;
 Matches 130; Conservative 100; Mismatches 251; Indels 171; Gaps 27;

OY 153 NAOCTDYRCHSALHAIERKSLOQCVKLLVENCANGANAHARACGRFPQGGCTCFYFGLP 212
 DB 62 NINOTDEPMNR--SALISAIENENEDLWILLEHNEIV-----GDALLHAISEEY 108
 OY 213 LSLAACKOMDVSYLLENPHQASIQATDSQNTV---LHALWISDNGSENALVTSM 269
 DB 109 VEAVEELLQWEETHN---KEGQPSWEAVDRSKSTFTVDITPLLAHRNVEELKI-- 162
 OY 270 YDGLAQAGARL-----CPVQLED-----INLQDLPLKLAAREGK 306
 DB 163 ---LDDGATILPMHPDYKCGDECVTSQTTDSLHNSOSRIATYALSSIALSSRPV 219
 OY 307 IEIPIHLLQREFSGLSHLSRKTETECYGVAVSLYDLAS--VDSCEENVLEITAFHCKS 364
 DB 220 LTFVQ--LSMELKRIQAMESEFRAE--YTEMKQVQDFGTSLLDHARTSMELVMLNENHE 276
 OY 365 P-----HHRRAVLEP--LNLKLAQKWLILKF----- 391
 DB 277 PSHDIWLGOROTLERKLAIIRYKQKFEVAHPVQOALLATWYDGLPFRKQASQOQMD 336
 OY 392 FLNFIACMLIYFIPTAVAYHOPTKKQAAHPHKAENSMMLTGHILHLLGILVVGOL 451
 DB 337 VVKIGCSFPIYSKLVIILADPDEGAKFMKRPVKFTTHSCSM--FPLMLGAASLRVQI 394
 OY 452 -----WVF-----NRRH-----VF-----I 461
 DB 395 TFELLAPPMWLTLEDRKHERGSLPPIELAITTYIMALIFEELKSLYSDGLFEYIMDL 454
 OY 462 W--ISFIDSYFEILFLF--QALLTVVSGVLCETLAIEWL-----PLIVS-----A 502
 DB 455 WNIYDYSNNMYTWIILCRATAMVIYHNDLWFRGIDPFPREHHPDPMLLSGACAPAG 514
 OY 503 LVLAGMLLVYTRGFOHTGTIYSVMIOKVIILDLRFLIYLVPLFGPAVALVLSQEMR 562
 DB 515 MVEFYKLAVHFFSINPHGLQVSLGRMII-DIKFFIYIVLVFARG---CGLNQLLMY 570
 OY 563 PEAPFGNATESVQPMESQDEGNGA---QYRGILEASLELFTITGMELAFQE-- 614
 DB 571 -YAELEKNCYHLDVADFPDQDEKACTIWRFRFNLFEFSQSLFMAFSGVLVDFDIAG 629
 OY 615 -QHFHFGMVLILLAYVLLYLLIILNMLIAMSETVNSVATDSIMKQLQA 665
 DB 630 IKSFTREWALLMGYSYVINITVLLNMLIAMMSNVOIISERADTEWKFARS 681

RESULT 3
 TRPL_DROME STANDARD; PRT; 1124 AA.
 AC P48994;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE TRANSLANT-RECEPTOR-POTENTIAL LIKE PROTEIN.
 GN TRPL.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;

RX MEDLINE=92232293; PubMed=1314616;
 RA Phillips A.M., Bull A.L., Kelly L.E.;
 RT "Identification of a Drosophila gene encoding a calmodulin-binding
 RT protein with homology to the trp phototransduction gene.";
 RL Neuron 8:631-642(1992).
 CC -1- FUNCTION: BINDS CALMODULIN. SUGGESTED TO MEDIATE CALCIUM ENTRY.
 CC SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT CHANNEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHADOMERIC
 CC MEMBRANES OF THE PHOTORECEPTOR CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 ANK REPEATS.
 CC
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DR EMBL: M88185; AAA28979.1; -.
 DR FlyBase: Fbgn0005614; trpl.
 DR InterPro: IPR002110; -.
 DR InterPro: IPR002153; -.
 DR Pfam: PF00023; ank. 2.
 DR PRINTS: PR01097; TRNSRRECEPTR.
 DR PROSITE: PSS0088; ANK_REPEAT. 1.
 DR PROSITE: PSS0297; ANK_REPEAT. 1.
 DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW Calmodulin-binding; Vision; ANK repeat; Repeat.
 FT TRANSMEM 341 361 POTENTIAL.
 FT TRANSMEM 374 394 POTENTIAL.
 FT TRANSMEM 432 452 POTENTIAL.
 FT TRANSMEM 513 533 POTENTIAL.
 FT TRANSMEM 549 569 POTENTIAL.
 FT TRANSMEM 609 629 POTENTIAL.
 FT TRANSMEM 646 666 POTENTIAL.
 FT REPEAT 78 107 ANK 1.
 FT REPEAT 152 181 ANK 2.
 FT DOMAIN 710 727 CALMODULIN-BINDING (POTENTIAL).
 FT DOMAIN 809 825 CALMODULIN-BINDING (POTENTIAL).
 SQ SEQUENCE 1124 AA; 127697 MW; E14796D5A2C10BD CRC64;

Query Match 4.9%; Score 197.5; DB 1; Length 1124;
 Best Local Similarity 19.7%; Pred. No. 2.2e-06;
 Matches 162; Conservative 130; Mismatches 281; Indels 249; Gaps 38;

OY 131 VNACILPLQIDRSGNPOL-----VNAOCTDD 159
 DB 25 VGGCCVPL-----GLPQLLEEKFFLAVERGDMPNVRRIQKALRHQHININMDP 77
 OY 160 YRRGSHALHAIERKSLOQCVKLVENG---ANVHARAC-----GRFQKG 201
 DB 78 L--GRRALTILADINENEMVELLVVGVETKDALHAIINAEFVAVELLEHEELIKEG 135
 OY 202 Q-----GTCFYGEL--PLSLAACKOMDVSYLEN-----PH-----QPSAL 238
 DB 136 EPPYSQKVDINTAMFADITPLMLAARKNNFEILRIILDRGAAPVPHDIRGCECEVRL 195
 OY 239 QATDSQNTVLA-----ALWISDNGSENALVTSMYDGLAQAGARLCPVQLED 288
 DB 196 TAEBSLHSLSRVNIYALCPSLICLSNPPSTATQLSMELRNALITBECKSEYMDL 255
 OY 289 IRNLQ-----DIFPLKLAAREGKIEI-----FRHILQREFSGLSHLSRKTETEC 332
 DB 256 RROCKRAVVDLDDOTRHSNELAILNVDPMQSYEPDPMSTFRLVOAISYKQKFF--A 313
 OY 333 YGPVRSVL---YDLAVSDCEENVLEITAFHCKSPHRRHNVLEPLINKL---QAK 383
 DB 314 HSNIQQLLSIWD--GLPGFRRSIVDKYI--CIA-----QVAVLPLCYLITWACADNCR 365

QY 384 MDLIRPFLNLCN-----LYMFIFTAVA-----YHOPFLKQAAPHKAEVGN 429
 CC 366 TQGLMKRPFKFLHASSYLFELILVQSARDDFVRIFGTTRMKKELEQELRQCG 425
 Db 430 SMLTGHILLIGITLVNQGLWYFRRHVFIMISFIDSFELLFLFOALL--TVSQVL 487
 QY 426 ---TPSKLELIVMTV---IGFWEEVOEIVAVGSKSLRNMNMTIDLRNSLYSVM 477
 Db 488 CFLAIEW-----YLP-----LLVASLVGMLNLYTRGFG 518
 QY 478 CLNAPAYIQOATEIARDPOKAYIPREKMHDFDQLAEGFLAANAYFSALKLVHLSINP 537
 Db 519 HTGITYSVMIQKVLRLDLRLLYLVFLGFAVALYSLOEAM-----RPEAPGPNAT 572
 QY 538 HLGEPQISLGRWVI-DIVKFFFLYTLVLFVFA---CGLNOLWYFPALEKSKCYVLP-- 591
 Db 573 ESYQPMGGOEDEGNGA-----QYRGILEASLELFFGTGMDL-----AROEOLHFR 619
 QY 592 -----GEADMGSHGDSCKMRFRGNLFSSOSLFWASGAMGLDFELSGIKSTTRFW 644
 Db 620 GAVLLLLAVLLTYLLMLTALMSETVNSVATDSWISWIKLQKAI SVLEMENGYWCR 679
 QY 645 G-LMGESYSVINIVLNLITAMMSNSYAMIDEHSDTEMKFAR-----TKLMMSY 694
 Db 680 KKRAGVMTLVGKPKPGSPDERKCFV-----EEYNWASWQTLPTLC 722
 QY 695 FEDSA---TLPPFVNLPSVKVIRIFRKSXTIDRORSKRRKEOEFOEYNIMKSLV 750
 QY 723 EDPSGAVPRTLENPVLASPKDE--DGASENYPVOLLQ 762
 Db 751 W-RYVAAMHRKFEEN---NPVSEDDINEVKSLEINTMRYEMLE 787

RESULT 4
 TRPL_MOUSE STANDARD: PRT: 809 AA.
 AC 061056; 035722; 40, Created)
 DT 01-OCT-2000 (Rel. 40, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE TRANSPARENT RECEPTOR POTENTIAL CHANNEL 1 (TRANSPARENT RECEPTOR PROTEIN 1)
 DE (MTRPL) (TRP-RELATED PROTEIN 1).
 GN TRPCL OR TRPPL OR TRPL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=insulinoma; PubMed-9165220;
 RA Sakura H., Ashcroft F.M.;
 RT Identification of four trpl gene variants murine pancreatic beta-cells.
 RL Diabetologia 40:528-532(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (BETA ISOFORM).
 RC TISSUE=Lens epithelium;
 RA Rae J.L.;
 RT Ion channels in lens epithelia.
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 551-615 FROM N.A.
 RA MEDLINE=96234226; PubMed-8646775;
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
 RA Birnbaumer L.;
 RT A novel mammalian gene family essential for agonist-activated
 RT capacitatively Ca2+ entry.
 RL Cell 85:661-671(1996).
 CC -1- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TRANSPARENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 ANK REPEATS.
 CC -----
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 CC or send an email to license@isb-stb.ch).
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DR EMBL: U73625; AAB50622.1; -
 DR EMBL: U95167; AAC53162.1; -
 DR EMBL: AF191551; AAF05725.1; -
 DR EMBL: U40980; AAC52699.1; -
 DR MGD: MGI:109528; Trpl.
 DR InterPro: IPR002113; -
 DR InterPro: IPR002153; -
 DR PRINTS: PRO1097; TRNSRCEPTRP.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW ANK repeat; Repeat; Alternative splicing.
 FT TRANSMEM 367 POTENTIAL.
 FT TRANSMEM 403 POTENTIAL.
 FT TRANSMEM 432 POTENTIAL.
 FT TRANSMEM 452 POTENTIAL.
 FT TRANSMEM 512 POTENTIAL.
 FT TRANSMEM 556 POTENTIAL.
 FT TRANSMEM 603 POTENTIAL.
 FT TRANSMEM 623 POTENTIAL.
 FT TRANSMEM 633 POTENTIAL.
 FT REPEAT 62 91 ANK 1.
 FT REPEAT 99 128 ANK 2.
 FT REPEAT 174 203 ANK 3.
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 597 597 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 126 159 MISSING (IN ISOFORM BETA).
 SQ SEQUENCE 809 AA; 92727 MW; DFD8377D5C538CDD CRC64;

Query Match 4.0%; Score 159; DB 1; Length 809;
 Best local Similarity 18.8%; Pred. No. 0.00083;
 Matches 142; Conservative 115; Mismatches 249; Indels 248; Gaps 34;

QY 86 GVEDIAGLPEY-----LSKTSKYLTDEYEGSGTKCLMKAV----- 124
 Db 2 GAPPSPGLPSPNAMAALYPTDLSGVSSSLSPSSSPSSPNEVMALKDVREKENT 61
 QY 125 LNKDGVNAC-----ILPLQIDRDGSGNPPVLNAOCTDYYRGHSALHIAIERRSIQ 177
 Db 62 LNEKFLFLACDKGDYVWKILE-ENSSGD---LNINCVD--VLGRNAVITITENESID 114
 QY 178 CAVLVENAGN-----VHARAG-----RFPKGGCGCFRFG----- 210
 Db 115 ILQLLDYGCQSADALLVAIDSEVGVAVDILNHRKRSSPTIVKLMERIONPEYSTM 174
 QY 211 --LPLSLACTKQMDVSYLLE--NPH----- 233
 Db 175 DVAPVILAAHRNRYETLTMILKODVSLPRHVGCECTCSAKNKKDSLHRSFRIDIR 234
 QY 234 ---QPASIQATDSQNTVLHAIWMISD-----NSAENIALVTSMYDGLLQQA 278
 Db 235 CLASPALIMLTEE--DPIILAFELADLKELSVEVEFRNDYEELARQCKMFKADLLQA 292
 QY 279 RLCPTVQLEDIRN-----LQDITPLKLAKBEKIEFIHIIQORESGIS 322
 Db 293 R--NSRELEVILNHTSSDPELKGILLERRMNLSRLKAIKYN-----QKE- 337
 QY 323 HLSRKTEMCYGVAVSLVDLASVDSCEENSVLEIIAFCKSPHRR-----MVLE-- 374
 Db 338 -----VSQSKCQ--PLNTYWFQMSGRKRPCKIKIMYLVIG 374

QY 375 ---PUNKL-----QAKWDLIPKFFLNCNLIYMFET-----AVAYHQPPLKKQAA 420
DQ 375 IFWVLSTCYLIAPKSOFGRIIHPKFIHGASYSFILLNLYSLVNEDEK----- 428
QY 421 PHLAECNSNLLGHILLGLGTYLVGOLMFMRRVFWISIDSYFE-----ILFL 475
DQ 429 ---KNTWMPALERIDYLLT-----WIIGMTWSDIKR---LWYEGLEDFLESRNQSLSFV 477
QY 476 FQA---LTVVLSQVLCFLAI-----EW---YLPLVLSALVGMNLLLYTGTGFGHTGIS 524
DQ 478 MNSLYLATFALKVYAHNKHDFADRKMDAPHPLVAGLEAFANVLSYLLFPHYTTSS 537
QY 525 VM-----IQVILRDLEFLLIYVLFEGFVALVSLSQEAMRPAPTGPMTATESVQDME 579
DQ 538 ILGFLQISMGMQLADFGFKLMPFLVLFSSFTIGLTQDKGY-----TSKEDQKCVGJFC 592
QY 580 GDEEGNAGVARGILEASLEKFTIGMGLAF-----QEQULHFGWVLLLLLAIVL 631
DQ 593 EEOGNDT---FHSFTGTCFALFWYFSLAHVAIFVTRPSYGELOSFGAV--IVGTYNV 647
QY 632 LTVILLNMLIALMSEYVNSVATDSWSIMKLOKA 665
DQ 648 VVVIVLTKLVAMLMKRSQOLLANHDEKMKRARA 681
RESULT 5
ID ANK2_HUMAN STANDARD; PRT: 3924 AA.
AC 001484: 001485:
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RA MEDLINE=94075409; PubMed=8253844;
RA Chan W., Kordell E., Bennett V.,
RT "440-kD ankyrin: structure of the major developmentally regulated
RT domain and selective localization in unmyelinated axons.";
RL J. Cell Biol. 123:1463-1473(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RA MEDLINE=91302466; PubMed=1830053;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.,
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).
RN [3]
RP REVISIONS.
RA Carpenter S.,
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 463-495 FROM N.A.
RA MEDLINE=92009921; PubMed=1833308;
RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.,
RT "Isolation and chromosomal localization of a novel noneythrinoïd
RT ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
CC SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
CC BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,
CC AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
CC DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
CC THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN.
CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
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DR EMBL; X56957; CAA40278.1; -
DR EMBL; X56958; CAA40279.2; -
DR EMBL; M37123; AAA62828.1; -
DR PIR; S14533; S14533.
DR PIR; A39643; A39643.
DR PIR; B39643; B39643.
DR PIR; S14569; S14569.
DR HSSP; 000420; IABC.
DR MIM; 106410; -
DR InterPro; IPR000488; -
DR InterPro; IPR000906; -
DR InterPro; IPR002110; -
DR Pfam; PF00791; Z05; 1.
DR Pfam; PF00023; ank; 22.
DR Pfam; PF00531; death; 1.
DR PROSITE; PSS0088; ANK_REPEAT; 20.
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW Phosphorylation; Multigene family.
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FT REPEAT 96 125 ANK 2.
FT REPEAT 129 158 ANK 3.
FT REPEAT 162 191 ANK 4.
FT REPEAT 193 220 ANK 5.
FT REPEAT 232 261 ANK 6.
FT REPEAT 265 294 ANK 7.
FT REPEAT 298 327 ANK 8.
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FT REPEAT 11369 11402 ANK 354.
FT REPEAT 11405 11434 ANK 355.
FT REPEAT 11437 11466 ANK 356.
FT REPEAT 11469 11502 ANK 357.
FT REPEAT 11505 11534 ANK 358.
FT REPEAT 11537 11566 ANK 359.
FT REPEAT 11569 11598 ANK 360.
FT REPEAT 11601 11630 ANK 361.
FT REPEAT 11633 11662 ANK 362.
FT REPEAT 11665 11694 ANK 363.
FT REPEAT 11697 11726 ANK 364.
FT REPEAT 11729 11758 ANK 365.
FT REPEAT 11761 11790 ANK 366.
FT REPEAT 11793 11822 ANK 367.
FT REPEAT 11825 11854 ANK 368.
FT REPEAT 11857 11886 ANK 369.
FT REPEAT 11889 11918 ANK 370.
FT REPEAT 11921 11950 ANK 371.
FT REPEAT 11953 11982 ANK 372.
FT REPEAT 11985 12014 ANK 373.
FT REPEAT 12017 12046 ANK 374.
FT REPEAT 12049 12078 ANK 375.
FT REPEAT 12081 12110 ANK 376.
FT REPEAT 12113 12142 ANK 377.
FT REPEAT 12145 12174 ANK 378.
FT REPEAT 12177 12206 ANK 379.
FT REPEAT 12209 12238 ANK 380.
FT REPEAT 12241 12270 ANK 381.
FT REPEAT 12273 12302 ANK 382.
FT REPEAT 12305 12334 ANK 383.
FT REPEAT 12337 12366 ANK 384.
FT REPEAT 12369 12402 ANK 385.
FT REPEAT 12405 12434 ANK 386.
FT REPEAT 12437 12466 ANK 387.
FT REPEAT 12469 12502 ANK 388.
FT REPEAT 12505 12534 ANK 389.
FT REPEAT 12537 12566 ANK 390.
FT REPEAT 12569 12598 ANK 391.
FT REPEAT 12601 12630 ANK 392.
FT REPEAT 12633 12662 ANK 393.
FT REPEAT 12665 12694 ANK 394.
FT REPEAT 12697 12726 ANK 395.
FT REPEAT 12729 12758 ANK 396.
FT REPEAT 12761 12790 ANK 397.
FT REPEAT 12793 12822 ANK 398.
FT REPEAT 12825 12854 ANK 399.
FT REPEAT 12857 12886 ANK 400.
FT REPEAT 12889 12918 ANK 401.
FT REPEAT 12921 12950 ANK 402.
FT REPEAT 12953 12982 ANK 403.
FT REPEAT 12985 13014 ANK 404.
FT REPEAT 13017 13046 ANK 405.
FT REPEAT 13049 13078 ANK 406.
FT REPEAT 13081 13110 ANK 407.
FT REPEAT 13113 13142 ANK 408.
FT REPEAT 13145 13174 ANK 409.
FT REPEAT 13177 13206 ANK 410.
FT REPEAT 13209 13238 ANK 411.
FT REPEAT 13241 13270 ANK 412.
FT REPEAT 13273 13302 ANK 413.
FT REPEAT 13305 13334 ANK 414.
FT REPEAT 13337 13366 ANK 415.
FT REPEAT 13369 13402 ANK 416.
FT REPEAT 13405 13434 ANK 417.
FT REPEAT 13437 13466 ANK 418.
FT REPEAT 13469 13502 ANK 419.
FT REPEAT 13505 13534 ANK 420.
FT REPEAT 13537 13566 ANK 421.
FT REPEAT 13569 13598 ANK 422.
FT REPEAT 13601 13630 ANK 423.
FT REPEAT 13633 13662 ANK 424.
FT REPEAT 13665 13694 ANK 425.
FT REPEAT 13697 13726 ANK 426.
FT REPEAT 13729 13758 ANK 427.
FT REPEAT 13761 13790 ANK 428.
FT REPEAT 13793 13822 ANK 429.
FT REPEAT 13825 13854 ANK 430.
FT REPEAT 13857 13886 ANK 431.
FT REPEAT 13889 13918 ANK 432.
FT REPEAT 13921 13950 ANK 433.
FT REPEAT 13953 13982 ANK 434.
FT REPEAT 13985 14014 ANK 435.
FT REPEAT 14017 14046 ANK 436.
FT REPEAT 14049 14078 ANK 437.
FT REPEAT 14081 14110 ANK 438.
FT REPEAT 14113 14142 ANK 439.
FT REPEAT 14145 14174 ANK 440.
FT REPEAT 14177 14206 ANK 441.
FT REPEAT 14209 14238 ANK 442.
FT REPEAT 14241 14270 ANK 443.
FT REPEAT 14273 14302 ANK 444.
FT REPEAT 14305 14334 ANK 445.
FT REPEAT 14337 14366 ANK 446.
FT REPEAT 14369 14402 ANK 447.
FT REPEAT 14405 14434 ANK 448.
FT REPEAT 14437 14466 ANK 449.
FT REPEAT 14469 14502 ANK 450.
FT REPEAT 14505 14534 ANK 451.
FT REPEAT 14537 14566 ANK 452.
FT

QY 377 ----NKLQAKMDLIPKFLNLIYMFETAVAYHOPFLKQADPLKA-----EV 427
DB 572 AVHHNMLDVK--LLPR-----GGSPHSPAMNGTTPHIAKONQIEV 613
QY 428 GNSMLTGG 435
DB 614 ARSLLOYG 621

RESULT 8
TRP3_HUMAN STANDARD; PRT; 848 AA.
ID 013507; 000593; 015660;
AC 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TRANSIENT RECEPTOR POTENTIAL CHANNEL 3 (HTRP-3).
GN TRP3 OR TRP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96234226; PubMed-8646775;
RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
RA Birbaumer L.;
RT "trp, a novel mammalian gene family essential for agonist-activated
RT capacitative Ca2+ entry.";
RL Cell 85:661-671(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97358541; PubMed-9215637;
RA Xu X.-Z., Li H.-S., Guggino W.B., Montell C.;
RT "Coassembly of TRP and TRPL produces a distinct store-operated
RT conductance.";
RL Cell 89:1155-1164(1997).
RN [3]
RP SEQUENCE OF 632-747 FROM N.A.
RX TISSUE=Brain;
RA MEDLINE-96003837; PubMed-7568191;
RA Wes P.D., Chevesich J., Jeromin A., Rosenberg C., Stetten G.,
RA Montell C.;
RT "TRPL, a human homolog of a Drosophila store-operated channel.";
RT Proc. Natl. Acad. Sci. U.S.A. 92:9652-9656(1995).
CC -1- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).
CC -1- SEEMS TO FORM A CALCIUM PERMEANT CHANNEL.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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CC -----
DR EMBL: U47050; AAC51653.1; -
DR EMBL: Y13758; CAA74083.1; -
DR EMBL: X89068; CAA61448.1; -
DR MIM: 602345; -
DR InterPro: IPR002110; -
DR InterPro: IPR002111; -
DR InterPro: IPR002153; -
DR Pfam: PF00023; ank; 2;
DR PRINTS: PR01097; TRANSMEMBRANE; Ion transport; Calcium channel;
KV Ionic channel; Transmembrane; Ion transport; Calcium channel;
KV ANK repeat; Repeat; Glycoprotein.
FT TRANSMEM 350 370 POTENTIAL.
FT TRANSMEM 382 402 POTENTIAL.

FT TRANSMEM 431 451 POTENTIAL.
FT TRANSMEM 464 484 POTENTIAL.
FT TRANSMEM 536 556 POTENTIAL.
FT TRANSMEM 580 600 POTENTIAL.
FT TRANSMEM 616 636 POTENTIAL.
FT TRANSMEM 650 670 POTENTIAL.
FT REPEAT 38 67 ANK 1.
FT REPEAT 73 102 ANK 2.
FT REPEAT 104 130 ANK 3.
FT REPEAT 159 188 ANK 4.
FT CARBOHYD 337 337 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 416 416 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CARBOHYD 671 671 N-LINKED (GLCNAc. . .) (POTENTIAL).
FT CONFLICT 739 742 EMGM -> GNGEM (IN REF. 3).
SQ SEQUENCE 848 AA; 97354 MW; 1DBC92BC941DE416 CRC64;

Query Match 3.5%; Score 139; DB 1; Length 848;

Best Local Similarity 18.4%; Pred. No. 0.024;

Matches 128; Conservative 96; Mismatches 222; Indels 248; Gaps 32;

QY 152 VNAOCTDYYRGHSALHIAIEKRSIQCVKLV--ENGAVY-----HAR----- 192
DB 65 LVNVCVD--YMGONMLQIAGVGNHLEVTLLKKEKRLARIGDALLAYSQGVRYVEAIL 122
QY 193 -----ACGRFQKG-----OGNCFYFGLPLSLACTQKMDVSYLL-- 229
DB 123 NHPGFAKRLTLSPCEQLQDDDFRAYDEDDGTRSPDITPILAAHCKQYEVYHMLMK 182
QY 230 ---ENPH-----OPASLOANDSOGNTVLAHV 253
DB 183 GARIEPHDYFCCKGDCMEKORHDSFSRSRLNAYKGLASPAVLSL--SSDDPVLTAL 240
QY 254 MISDMSAENIALVTSMD-----GLLAGARLC-PRVQLEDIRN--LQDL 295
DB 241 L--SNEKLARIANIEKEFKNDYRKLSMOCKDFVGVYLD--LCRDESEVEALINDLESA 294
QY 296 TPPLKLAAGKLEIFRH--ILOREFSGLSHLRKPFEM--CYGPVRSYLDIASVDSCE 351
DB 295 EPL-----EVRHKASLSRVKLAIEYVKKFAVHNCQOOLITTYE--NLSGLRE 343
QY 352 NSVLEIIFAHCKSPHRRHNVV-----EPLNKLQAKMDLIPKFL 393
DB 344 ----QTIATKC-----LVVLVVALGLPFLAIGVWIAPCSRLGILRSP-----FM 384
QY 394 NFLCNLIYFITTAVAYHO-----PLKQADPHLKAEGVNSMLTGHILIL-- 440
DB 385 KEVAHAASFLIFGLLVFNASDRFEGITTLPNITVYDYPKQIFRKVTOFTWTEMLIMW 444
QY 441 -LGGIYILAVGOLWY-----FMRHRYFI-----WISF-----IDSY 469
DB 445 VLGMMSEKELMEGPREYIIQLNVLDFGMLSTIFIAFTARFLAFLQATQAQYVDSY 504
QY 470 FEILFLQALLTVVSQVLCFIAIEWLP-----LLVASLVGLWLLLYYTGPFQHT 520
DB 505 VQESDLSVETLPEIQVFTYARDKW-LPSDPOITSEGLVAIVLWFSRIAYILPANESF 563
QY 521 GIYSWAIQVILRDLRLPLLIYLVLFGRFAVALVLSQGAMPPEAPGTGNANESVQPMG 580
DB 564 GPLQISLGRTY-KDIFKEVNLFIWFFAFMIGMFTLISYLGAKV----- 607
QY 581 QDEDEGAYRGILFASLELFKFTIGMGLA-----FOEQLHFRGMVLLLLAYVL 631
DB 608 -----NAFTVESSEKFLFSTIGLSVTVLKYDKHFIENIGY-----VLGIYIV 656
QY 632 LPTIILLNMLLIMSETVNSVATDSMSIWLQKA 665
DB 657 TMVVVLLNMLIMINSVQEIDDSDVEKFKPARS 690

RESULT 9

ID	ANK1_HUMAN	STANDARD:	PRT: 1880 AA.
AC	P16157;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-APR-1990 (Rel. 14, Last sequence update)		
DT	01-OCT-2000 (Rel. 40, Last annotation update)		
DE	ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRIN 2.1 AND 2.2).		
GN	ANK1 OR ANK.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_Taxid:9606;		
RN	[1]		
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS.		
RC	TISSUE-Hematopoietic;		
RA	MEDLINE=90158830; PubMed=2137557;		
RA	Lux S.E., John K.M., Bennett V.;		
RT	"Analysis of cDNA for human erythrocyte ankyrin indicates a repeated		
RT	structure with homology to tissue-differentiation and cell-cycle		
RT	control proteins.";		
RL	Nature 344:36-42(1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90175370; PubMed=1689849;		
RA	Lambert S., Yu H., Pichal J.T., Lawler J., Ruff P., Speicher D.,		
RT	Cheng M.C., Kan Y.W., Palek J.;		
RT	"cDNA sequence for human erythrocyte ankyrin."		
RL	Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).		
RN	[3]		
RP	VARIANT HS ILE-462.		
RA	MEDLINE=9625450; PubMed=8640229;		
RA	Eber S.W., Gonzalez J.M., Lux M.D., Scarpa A.L., Tse W.T.,		
RA	Dornweller M., Herbers J., Kugler W., Oezcan R., Pekrun A.,		
RA	Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.;		
RT	"Ankyrin-1 mutations are a major cause of dominant and recessive		
RT	hereditary spherocytosis."		
RL	Nat. Genet. 13:214-218(1996).		
CC	-1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL		
CC	ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO		
CC	NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE		
CC	CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.		
CC	ERYTHROCYTE ANKIRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE		
CC	CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;		
CC	THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.		
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC		
CC	PLASMA MEMBRANE.		
CC	-1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY		
CC	ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN		
CC	VARIANT 2.1.		
CC	-1- PTM: REGULATED BY PHOSPHORYLATION.		
CC	-1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).		
CC	-1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE		
CC	HEREDITARY SPHEROCYTOSIS (HS).		
CC	-1- SIMILARITY: CONTAINS 23 ANK REPEATS.		
CC	-----		
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
DR	EMBL: X16609; CAA34610.1; -		
DR	EMBL: M28880; AAA51732.1; -		
DR	PIR: S08275; SJHUK.		
DR	PIR: A35049; A35049.		
DR	HSP: Q00420; IAMC.		
DR	MIM: 182900; -		
DR	InterPro: IPR000448; -		
DR	InterPro: IPR000906; -		
DR	InterPro: IPR002110; -		
DR	Pfam: PF00791; Z05; 1.		

DR	Pfam: PF00023; ank: 22.	
DR	Pfam: PF00531; death: 1.	
DR	PROSITE; PS50088; ANK_REPEAT: 20.	
DR	PROSITE; PS50297; DEATH_DOMAIN: 1.	
KW	Cytoskeleton: Alternative splicing: Repeat; ANK repeat;	
KW	Phosphorylation: Lipoprotein: Multigene family; Disease mutation;	
KW	Elliptocytosis: Polymorphism.	
FT	DOMAIN	1 826
FT	DOMAIN	827 1381
FT	DOMAIN	1382 1880
FT	REPEAT	43 72
FT	REPEAT	76 105
FT	REPEAT	109 138
FT	REPEAT	142 171
FT	REPEAT	173 200
FT	REPEAT	204 233
FT	REPEAT	237 266
FT	REPEAT	270 299
FT	REPEAT	303 332
FT	REPEAT	336 365
FT	REPEAT	369 398
FT	REPEAT	402 431
FT	REPEAT	435 464
FT	REPEAT	468 497
FT	REPEAT	501 530
FT	REPEAT	534 563
FT	REPEAT	567 596
FT	REPEAT	600 629
FT	REPEAT	633 662
FT	REPEAT	666 695
FT	REPEAT	699 728
FT	REPEAT	732 761
FT	REPEAT	765 794
FT	DOMAIN	1402 1486
FT	VARSPPLIC	1512 1873
FT	VARSPPLIC	1874 1874
FT	VARSPPLIC	1849 1880
FT	VARIANT	20 20
FT	VARIANT	462 462
FT	VARIANT	618 618
FT	VARIANT	749 749
FT	VARIANT	844 844
FT	VARIANT	1391 1391
FT	VARIANT	1285 1285
FT	VARIANT	1591 1591
FT	VARIANT	1698 1698
FT	CONFLICT	229 229
FT	CONFLICT	1345 1345
FO	SEQUENCE	1880 AA: 206145 MW: 10555E7EFDICD28 CRC64;

Query Match	3.4%	Score 138;	DB 1;	Length 1880;
Best Local Similarity	22.8%;	Pred. No. 0.079;		
Matches	82;	Conservative	45;	Mismatches 122;
				Indels 110;
				Gaps 16.
OY	134 CILPLQLQDRD-----	SSNPQL-VNAQCTDYR-----	GHSA LHI	169

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Db 319 CVRLLQDAEIDITLDTLPLHVAHC--GHHRAVKVLLDKAKPNSBALNCFPLHI 376
QY 170 AIEKRSLQCYKLVENGANY-----HARACRFQKG--QGTCTYFG 209
Db 377 ACKNHVRLVLLKTCASIDAVTESGLTPLHVASFGCHLPYKNIILQRCASPNVSVKV 436
QY 210 ELPPLSLACTKQMDVSYLLENPHQASLOATDSQNTVJHALVMSIDNSAENIALVTSM 269
Db 437 ETPPLHMAARGHTEVAKYLLQN--KAKVNAKKDDOTPLHCAARIGH-----TNM 484
QY 270 YDGLLAGARLCPTVOLEDIRNIDITPLKLAKEGKIEIFPHILOREFSGLSLKRFT 329
Db 485 VKLLENNAN-----PNLATTAGHTPLHIAAREGHVETVLALKEKASOACWTKKGF 537
QY 330 EW-----CYGVRYS--LYDLASVDSCEENSYLEI-IAFHCKSPHRRMVYLEPLNKLQ 381
Db 538 PLHVAAYGVRAVELLERDAHPNAGKNGLPPLHVAHV---HNMLDIV-----584
QY 382 AKMDLIPKFEFLNCLIMYFTAVAYHQPTLKAQAAPHLKA-----EVGNSMLLTG 435
Db 585 ---KILLIPR-----GGSPHSPAMNGYTPPLHIAKAKOVAVASLLQYG 624

RESULT 10
LATA_LATMA STANDARD; PRT; 1401 AA.
AC P23631:
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ALPHA-LATROTOXIN PRECURSOR.
OC Latrodectus mactans (Black widow spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneidae; Theridiidae; Latrodectus.
OC NCBI_TaxId=6924;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TREDECINGUTTATUS; TISSUE-Venom;
RX MEDLINE-91362695; PubMed-1977615;
RA Kiyatkin N.I., Duhobova I.E., Chekhovskaya I.A., Grishin E.V.;
RT "Cloning and structure of cDNA encoding alpha-latrotoxin from black
RT widow spider venom."
RL FEBS Lett. 270:127-131(1990).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE-91362695; PubMed-1888339;
RA Volkova T.M., Galkina T.G., Kudelin A.B., Nazimov I.V., Grishin E.V.;
RT "Structure of clyptic fragments of a neurotoxin from black widow
RT spider venom."
RL Bioorg. Khim. 17:437-441(1991).
CC -1- FUNCTION: CAUSES SYNAPTIC VESICLES EXOCYTOSIS AND
CC NEUROTRANSMITTER RELEASE FROM PRESYNAPTIC NERVE TERMINALS.
CC -1- PPM: ALPHA-LATROTOXIN MAY BE PROCESSED AT ITS C-TERMINUS.
CC -1- SIMILARITY: CONTAINS 21 ANK REPEATS.
DR PIR; S11527; S11527.
DR HSSP; Q00420; IAWC.
DR InterPro; IPR002110; -.
DR Pfam; PR00023; ank; 17.
DR PROSITE; PS50088; ANK_REPEAT; 11.
DR PROSITE; PS50297; ANK_REGION; 1.
KW Toxin; Neurotoxin; Repeat; ANK repeat; Venom; Signal.
FT SIGNAL 1 20
FT CHAIN 1 1401 ALPHA-LATROTOXIN.
FT REPEAT 490 521 ANK 1.
FT REPEAT 525 559 ANK 2.
FT REPEAT 559 589 ANK 3.
FT REPEAT 593 622 ANK 4.
FT REPEAT 626 656 ANK 5.
FT REPEAT 660 690 ANK 6.
FT REPEAT 695 723 ANK 7.
FT REPEAT 729 758 ANK 8.
FT REPEAT 762 791 ANK 9.

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FT REPEAT 795 824 ANK 10.
FT REPEAT 828 857 ANK 11.
FT REPEAT 862 891 ANK 12.
FT REPEAT 895 924 ANK 13.
FT REPEAT 928 957 ANK 14.
FT REPEAT 971 1003 ANK 15.
FT REPEAT 1003 1033 ANK 16.
FT REPEAT 1035 1064 ANK 17.
FT REPEAT 1068 1097 ANK 18.
FT REPEAT 1101 1131 ANK 19.
FT REPEAT 1137 1166 ANK 20.
FT REPEAT 1170 1199 ANK 21.
SQ SEQUENCE 1401 AA; 156834 MW; 21CE198B80172568 CRC64;

Query Match 3.4%; Score 134.5; DB 1; Length 1401;
Best Local Similarity 20.1%; Pred. No. 0.097; Indels 89; Gaps 13;
Matches 69; Conservative 62; Mismatches 123;

QY 35 GLPPMESQFQGEGR---KFAPIQIRVNLNRYRKT-----GASOPD 70
Db 594 GTPPLHAIATNGERILEAFNLQISIDVNAKSNGLPPLHAIITKNDMPVASTLLGSKVD 653
QY 71 PNRPRDRLEFNAVSRGVPEDLAIPYLKSKTSKYLRDSEYTESGKTCLMK---AVLN 126
Db 654 INAVDENNI-----TALHYAAILGLYETTKOLINLKEINAVVSPGLLSALHYAIIY 706
QY 127 LKGVANACILPPLQIDRDSNPQPLVNAOCTDYYGHSALHAIKRSIQCYKLVENG 186
Db 707 KHDVASFILRRSSNVN-----VNLKALG---GTPPLHAIYIGRRQILSMFDIG 753
QY 187 ANYHARACGRFQGGGTCTCFEGELPLSLACTKQMDVSYLLENPHQASLOATDSQGN 246
Db 754 VNIEQGTDEKY-----TPLHLAAMSKYVELIQLD---QGSNFEAKTNSGA 797
QY 247 TVLH-----ALVMSID-----NSAEN--TALVTSMYDGLQ-AGARLCPTVOLED 288
Db 798 TPLHLATFKGKSOAALILNLNENVMWRDDENGMPHIGAMTCLLVAQAIISIDATVVD 857
QY 289 IRLNQLTPLKLAKEGKIEIFPHILO-----REFSGLSHL 324
Db 858 IEDKNSDTPLNLAONSHDIVITFDQCADITFRKKGLAPL 900

RESULT 11
YAZA_SCHPO STANDARD; PRT; 642 AA.
ID YAZA_SCHPO
AC Q09701;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHETICAL 72.5 KDA PROTEIN C2F7.10 IN CHROMOSOME 1.
GN SPAC2F7.10.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxId=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (JUL-1995) to the EMBL/Genbank/DDb databases.
CC -1- SIMILARITY: NO YEAST AKR1.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC -----
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FT	DOMAIN	273	350	EGF-LIKE 7,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	311	350	EGF-LIKE 8,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	352	388	EGF-LIKE 9,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	389	427	EGF-LIKE 10,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	429	470	EGF-LIKE 11,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	472	508	EGF-LIKE 12,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	510	546	EGF-LIKE 13,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	548	584	EGF-LIKE 14,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	586	622	EGF-LIKE 15,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	622	656	EGF-LIKE 16,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	658	686	EGF-LIKE 17,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	688	724	EGF-LIKE 18,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	726	762	EGF-LIKE 19,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	764	800	EGF-LIKE 20,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	803	839	EGF-LIKE 21,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	841	877	EGF-LIKE 22,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	878	924	EGF-LIKE 23,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	926	962	EGF-LIKE 24,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	964	1000	EGF-LIKE 25,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1002	1040	EGF-LIKE 26,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1042	1081	EGF-LIKE 27,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1083	1122	EGF-LIKE 28,	CALCIUM-BINDING (POTENTIAL)
FT	DOMAIN	1126	1167	EGF-LIKE 29,	CALCIUM-BINDING (POTENTIAL)
FT	REPEAT	1168	1208	LIN/NOTCH 1,	CALCIUM-BINDING (POTENTIAL)
FT	REPEAT	1209	1242	LIN/NOTCH 2,	CALCIUM-BINDING (POTENTIAL)
FT	REPEAT	1243	1282	LIN/NOTCH 3,	CALCIUM-BINDING (POTENTIAL)
FT	REPEAT	1628	1657	ANK 1,	CALCIUM-BINDING (POTENTIAL)
FT	REPEAT	1661	1691	ANK 2,	CALCIUM-BINDING (POTENTIAL)
FT	REPEAT	1695	1724	ANK 3,	CALCIUM-BINDING (POTENTIAL)
FT	REPEAT	1728	1757	ANK 4,	CALCIUM-BINDING (POTENTIAL)
FT	REPEAT	1761	1790	ANK 5,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	25	38	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	32	48	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	50	59	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	65	77	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	71	100	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	102	111	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	119	130	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	124	140	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	142	151	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	157	168	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	162	177	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	179	188	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	195	208	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	202	217	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	219	228	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	235	246	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	240	259	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	261	270	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	277	288	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	282	297	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	299	308	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	315	329	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	323	338	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	340	349	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	356	367	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	361	376	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	378	387	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	393	404	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	398	415	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	417	426	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	433	449	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	443	458	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	460	469	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	476	487	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	481	496	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	498	507	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	514	525	BY SIMILARITY,	CALCIUM-BINDING (POTENTIAL)
FT	DISULFID	519	534	BY SIMILARITY,	CALCI

FT	DISULFID	590	601	BY	SIMILARITY.	
FT	DISULFID	595	610	BY	SIMILARITY.	
FT	DISULFID	612	621	BY	SIMILARITY.	
FT	DISULFID	626	637	BY	SIMILARITY.	
FT	DISULFID	631	646	BY	SIMILARITY.	
FT	DISULFID	648	655	BY	SIMILARITY.	
FT	DISULFID	662	669	BY	SIMILARITY.	
FT	DISULFID	664	674	BY	SIMILARITY.	
FT	DISULFID	676	685	BY	SIMILARITY.	
FT	DISULFID	692	703	BY	SIMILARITY.	
FT	DISULFID	697	712	BY	SIMILARITY.	
FT	DISULFID	714	723	BY	SIMILARITY.	
FT	DISULFID	730	741	BY	SIMILARITY.	
FT	DISULFID	735	750	BY	SIMILARITY.	
FT	DISULFID	752	761	BY	SIMILARITY.	
FT	DISULFID	768	779	BY	SIMILARITY.	
FT	DISULFID	773	788	BY	SIMILARITY.	
FT	DISULFID	790	799	BY	SIMILARITY.	
FT	DISULFID	807	818	BY	SIMILARITY.	
FT	DISULFID	812	827	BY	SIMILARITY.	
FT	DISULFID	829	838	BY	SIMILARITY.	
FT	DISULFID	845	856	BY	SIMILARITY.	
FT	DISULFID	850	865	BY	SIMILARITY.	
FT	DISULFID	867	876	BY	SIMILARITY.	
FT	DISULFID	882	903	BY	SIMILARITY.	
FT	DISULFID	897	912	BY	SIMILARITY.	
FT	DISULFID	914	923	BY	SIMILARITY.	
FT	DISULFID	930	941	BY	SIMILARITY.	
FT	DISULFID	935	950	BY	SIMILARITY.	
FT	DISULFID	952	961	BY	SIMILARITY.	
FT	DISULFID	968	979	BY	SIMILARITY.	
FT	DISULFID	973	988	BY	SIMILARITY.	
FT	DISULFID	990	999	BY	SIMILARITY.	
FT	DISULFID	1006	1019	BY	SIMILARITY.	
FT	DISULFID	1011	1028	BY	SIMILARITY.	
FT	DISULFID	1030	1039	BY	SIMILARITY.	
FT	DISULFID	1046	1057	BY	SIMILARITY.	
FT	DISULFID	1051	1069	BY	SIMILARITY.	
FT	DISULFID	1071	1080	BY	SIMILARITY.	
FT	DISULFID	1087	1098	BY	SIMILARITY.	
FT	DISULFID	1092	1110	BY	SIMILARITY.	
FT	DISULFID	1112	1121	BY	SIMILARITY.	
FT	DISULFID	1130	1142	BY	SIMILARITY.	
FT	DISULFID	1136	1155	BY	SIMILARITY.	
FT	DISULFID	1157	1166	BY	SIMILARITY.	

Query Match

Best Local Similarity 25.5%; Score 129; DB 1; Length 1964;

Matches 72; Conservative 37; Mismatches 103; Indels 70; Gaps 12;

Oy	94	LPEYLSKTSKYITDSEY-----TESGTGKTCIMKAV-----LNKIDVNACTPLLOIDRDS	145
Db	1553	LPOQAMLPPOECESESEVLDPDTCGPDGVTPLMSAVFCGCGVOSTGASPORLGL-----	1605
Oy	146	GNDPOP-----LVNAOCTDDVY--RGSHALHIALIENKSLQCVKLVNNGAN-----	188
Db	1606	GNLEEWPEPLLDGACGQQAHTVGTGETPLTLARFSPPTAARLLRLEGANPNQPPDAGRTP	1665
Oy	189	-----VHARACGRFFOKGQCTCF-----YFGLPLPLSLACTRQMDVSYLLENPHQOPASL	238
Db	1666	LHTVAADAARREVCOQLLASRQTSVDARFEDGTPPLMLARLAVEDLEBLLA---ARADY	1722
Oy	239	QATDSQGNVTVLHALVWISDNGSNAENTLALVTSMTDGLLOGARLCPTVVOLEDIRNLQDLPL	298
Db	1723	GARDRGKRTALMAAAYNNARAAR-----SLLOGAD-----KDAQDSREQTPPL	1766
Oy	299	KIAAKEGKIEIFRHILQ-----REFSGLS---HLSRKPTW 331	
Db	1767	FLAAREGAVEVAQOLLELLEGAANGFLDQAGLADGVAKORSHW 1808	

RESULT 14

SW14_YEAST

ID	SWI4 YEAST	STANDARD:	PRT: 1093 AA.
AC	P25302:		
DT	01-MAY-1992 (rel. 22, Created)		
DT	01-FEB-1995 (rel. 31, Last sequence update)		
DT	01-OCT-2000 (rel. 40, Last annotation update)		
DE	REGULATORY PROTEIN SWI4 (CELL-CYCLE BOX FACTOR, CHAIN SWI4)		
DE	(APR1 PROTEIN).		
GN	SWI4 OR APR1 OR YER111C.		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.		
OX	NCBI_TaxID=49332;		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=90098089; PubMed=2689885;		
RA	Andrews B.J., Herskowitz I.;		
RT	"The yeast SWI4 protein contains a present in developmental		
RT	regulators and is part of a complex involved in cell-cycle-dependent		
RT	transcription.";		
RL	Nature 342:830-833(1989).		
RL	[2]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=5288C / AB972;		
RA	Dierich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,		
RA	Aviles E., Beruo A., Brennan T., Carpenter J., Chen E., Cherry J.M.,		
RA	Chung E., Duncan M., Guzman E., Hartwell G., Hunnicke-Smith S.,		
RA	Hymen R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,		
RA	Moskale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,		
RA	Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,		
RA	Taylor P., Wei Y., Yelton M., Bortstein D., Davis R.W.;		
RL	Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases.		
RN	[3]		
RP	SEQUENCE OF 845-1093 FROM N.A.		
RX	MEDLINE=93360904; PubMed=8355657;		
RA	Daniel J.;		
RT	"Potentially rapid walking in cellular regulatory networks using the		
RT	gene-gene interference method in yeast.";		
RL	Mol. Gen. Genet. 240:245-257(1993).		
CC	-1- FUNCTION: PART OF A COMPLEX INVOLVED IN CELL-CYCLE-DEPENDENT		
CC	TRANSCRIPTION. SWI4 AND SWI6 ARE REQUIRED FOR FORMATION OF THE		
CC	CELL-CYCLE BOX FACTOR-DNA COMPLEX. THE REPEATED ELEMENT IN THE		
CC	UPSTREAM REGION OF HO (5'-CACGAAA-3') IS CALLED THE CELL CYCLE		
CC	BOX (CCB).		
CC	-1- SUBUNIT: SBF CONTAINS SWI6 AND SWI4.		
CC	-1- SIMILARITY: CONTAINS 2 ANK REPEATS.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration -		
CC	between the Swiss Institute of Bioinformatics and the EMBL collaboration -		
CC	the European Bioinformatics Institute. There are no restrictions on lists		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/sib.ch).		
CC	or send an email to license@sib-sib.ch).		
CC	-----		
DR	EMBL: X51606; CAA35949.1; -		
DR	EMBL: U18916; AAC03209.1; -		
DR	PIR: S07106; S07106.		
DR	PIR: S35260; S35260.		
DR	TRANSFAC: T00775; -		
DR	SGD: S0000913; SWI4.		
DR	InterPro: IPR002110; -		
DR	Pfam: PF00023; ank; 2.		
DR	PROSITE: PS50088; ANK_REPEAT; 2.		
DR	PROSITE: PS50297; ANK_REPEAT_REGION; 2.		
KW	Transcription regulation; DNA-binding; ANK repeat; Repeat.		
FT	DNA_BIND	37	138
FT	DOMAIN	201	727
FT	REPEAT	520	549
FT	REPEAT	641	670
FT	REPEAT	175	175
FT	CONFLICT	431	431
FT	CONFLICT	1054	1054
FT	CONFLICT	3	846
FT	MISSING (IN REF. 2).		

Seq	Sequence	1093 AA	123806 MW	40EA2EA7732687A9 CRC64
Query Match	3.28; Score 128.5; DB 1; Length 1093;			
Best Local Similarity	20.8%; Pred. No. 0.19;			
Matches 74; Conservative 48; Mismatches 134; Indels 99; Gaps				
Qy	10 FRLFTLGGGGDGGSEADRGKIDPFSSGLPRPMSQGGEDRKPAPQIRV-----	56		
Db	357 FNHSMDSITNGNSKKRRKKKTKQNSQ---EQDYYNOQEKIQRHFFKLMKQPLLMQSFQNP	411		
Oy	57 -----NLNRYKGTGASQDPDRPFDRDRLEFNAVSRGVEEDLAGLPEYLSKT	101		
Db	412 NDHNEKCDNSGNNNNNTVASNCSSTIEVPSSENDDNSMMSKMTPPFSAGNTSSONKL	471		
Oy	102 SKYLTDSERTEGSTGKTCLMKAVLNLDGVNACILPLLQIDRDSGNQPL-----	151		
Db	472 ENKMTDQEQK-----TILFTLSSRSRDVDQALLATLALYPAKN	510		
Oy	152 --VNAQCTDYIRGHSAHLIAIEKRSIQCVKLVANGANVAHARACGRF-FQKGQGTCTFF	208		
Db	511 FNINFEID--QCHTPLHMTAMANIPLKMLITTLNAN--ALQCNKIGFNCITKYSIEFN	565		
Oy	209 GELPLSLAACKQ--MPVSYLLNPNQPPASLQTSQGNVTVALMWDNSAENALY	266		
Db	566 N-----CKENAPDEIISILK-----ICLTTPDVNGRLPRFYLIELSVMKSNPMIT	612		
Oy	267 TSMYDG-LLAGQ-----ARLCPTVQLEDIRNLQDLTPPLKLAKEGKIEIFRHIL	314		
Db	613 KSYMDSITLSGGQDYNLKCKLCLWQ--DNIGN-----TPHLSALNLFVEYNNRLY	662		
RESULT 15				
NOTCH_DROME	NOTCH_DROME STANDARD; PRT; 2703 AA.			
AC	P07207; P04154;			
DT	01-NOV-1986 (Rel. 03, Created)			
DT	01-FEB-1996 (Rel. 33, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR.			
GN	N.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Braconyera; Muscomorpha;			
OC	Ephydroidae; Drosophilidae; Drosophila.			
OX	NCBI_TaxId=7227;			
RN	11			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=66079539; PubMed=3935325;			
RA	Wharton K.A., Johansen K.W., Xu T., Artavanis-Tsakonas S.;			
RT	"Nucleotide sequence from the neurogenic locus notch implies a gene			
RT	product that shares homology with proteins containing EGF-like			
RT	repeats.";			
RL	Cell 43:567-581(1985).			
RL	12			
RN	[2]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=OREGON-R;			
RC	MEDLINE=87064624; PubMed=3097517;			
RX	Kidd S., Kelley M.R., Young M.W.;			
RA	"Sequence of the notch locus of Drosophila melanogaster: relationship			
RT	of the encoded protein to mammalian clotting and growth factors.";			
RT	Mol. Cell. Biol. 6:3094-3108(1986).			
RL	13			
RN	SEQUENCE OF 2505-2611 FROM N.A.			
RP	MEDLINE=85099329; PubMed=2981631;			
RC	Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;			
RA	"opa: a novel family of transcribed repeats shared by the Notch locus			
RT	and other developmentally regulated loci in D. melanogaster.";			
RT	Cell 40:55-62(1985).			
RL	14			
RN	SEQUENCE OF 1-8 FROM N.A.			
RP	MEDLINE=87257846; PubMed=3037327;			
RC	Kelley M.R., Kidd S., Berg R.L., Young M.W.;			
RA				

FT	DISULFID	497	512	BY SIMILARITY.
FT	DISULFID	514	523	BY SIMILARITY.
FT	DISULFID	530	541	BY SIMILARITY.
FT	DISULFID	535	550	BY SIMILARITY.
FT	DISULFID	552	561	BY SIMILARITY.
FT	DISULFID	568	579	BY SIMILARITY.
FT	DISULFID	573	588	BY SIMILARITY.
FT	DISULFID	590	599	BY SIMILARITY.
FT	DISULFID	606	616	BY SIMILARITY.
FT	DISULFID	611	625	BY SIMILARITY.
FT	DISULFID	627	636	BY SIMILARITY.
FT	DISULFID	643	654	BY SIMILARITY.
FT	DISULFID	648	663	BY SIMILARITY.
FT	DISULFID	665	674	BY SIMILARITY.
FT	DISULFID	681	692	BY SIMILARITY.

Query Match 3.1%; Score 124.5; DB 1; Length 2703;
 Best Local Similarity 23.9%; Pred. No. 1.2; Mismatches 15;
 Matches 75; Conservative 47; Indels 77; Gaps 15;

QY	39	MESQFQEDRKFPQIRVNIYRKQ--TGASQDPNRFDRD-----LFNAVSRG--	86
DB	1856	WVSEYEADQRYWQAHLDVYVRAIMTPRAHQDGGKHVDARGPGCLTPIMIAVARGG	1915
QY	87	--VPEDLAGLPEYLSKTSKYLTD-----SEYEGSTGKTCIMKAVLNKQGVNACILP	137
DB	1916	LPTGEDIEENNED--STAQVISDLAOGAELNATMDKTGETSIHLAARFARADAKRL-	1971
QY	138	LQIDRDGNGPQVNVNACTDYYRGHSALHIAIEKRSLOCVKLVENG- NVHARACGR	196
DB	1972	-----DAG-----ADANCODN--TGRTPLHAADVADAGVFOILRNRAITNLAR----	2014
QY	197	FQKGGGTCFYEGELPLSLAACKQMDVVSYLENPHQPSLOATDSOGNTVLAHLMIS	256
DB	2015	-----MHDGTPPLILAARLAIEGWEDLIT--ADADRMAADNSGKTALHMAAVN	2062
QY	257	DNSAENIALVTSNYDGLLAGARLCTVQLEDIRNLQDILTPKLAKKEGKIETFRHIL--	314
DB	2063	NTEAVNI-----LIMHHAN-----RDADDKDETPPLAAREGSYENACKALDN	2106
QY	315	--QREFSGLSLSR	326
DB	2107	FANREIT--DHMDR	2118

Search completed: July 18, 2001, 16:00:28
 Job time: 131 sec